

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 4, 2002, 01:54:20 ; Search time 47.6067 Seconds
(without alignments)
1592.744 Million cell updates/sec

Title: US-09-805-550-4

Perfect score: 1910
Sequence: 1 MKLVKTLKGFHFELRVPN.....CDNEELANYLLLEHAGEED 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1169.5	61.2	365	10 094CE9	094CE9 arabidopsis
2	1153.5	60.4	379	10 003991	003991 daucus caro
3	1043.5	54.6	367	10 09MA10	09MA10 arabidopsis
4	1019	53.4	389	10 09STA6	09STA6 lycopersico
5	978	51.2	419	10 09M887	09M887 arabidopsis
6	954	49.9	382	10 003990	003990 daucus caro
7	931.5	48.8	378	10 09FE16	09FE16 arabidopsis
8	930.5	48.7	378	10 094C35	094C35 arabidopsis
9	887.5	46.5	392	10 040742	040742 oryza sativ
10	861.5	34.6	246	10 09S918	09S918 arabidopsis
11	621.5	32.5	409	4 08W0B0	08W0B0 homo sapien
12	490.5	25.7	414	5 09XZE0	09XZE0 drosophila
13	487.5	25.5	414	5 09V3W9	09V3W9 drosophila
14	484	25.3	341	5 097135	097135 dictyostel
15	424	22.2	113	5 09SA20	09SA20 arabidopsis
16	405	21.2	372	5 023451	023451 caenorhabd1

17	405	21.2	748	6 P79370	P79370 oryctolagus
18	375	19.6	230	5 09VCD5	09VCD5 drosophila
19	215	11.3	523	5 09NIF3	09NIF3 dictyostel
20	214	11.2	575	10 09EFM5	09EFM5 oryza sativ
21	204.5	10.7	142	10 09LE19	09LE19 arabidopsis
22	201	10.5	551	10 09S118	09S118 arabidopsis
23	201	10.5	551	10 094C51	094C51 arabidopsis
24	194.5	10.2	538	10 09S119	09S119 arabidopsis
25	193	10.1	65	10 09SCA8	09SCA8 lycopersico
26	180.5	9.5	582	11 09QZM1	09QZM1 mus musculus
27	176	9.2	589	4 09H0T8	09H0T8 homo sapien
28	176	9.2	589	4 09UMX0	09UMX0 homo sapien
29	174	9.1	595	6 09S5M9	09S5M9 bos taurus
30	171	9.0	601	4 09NRR5	09NRR5 homo sapien
31	170.5	8.9	582	11 09JUP9	09JUP9 rattus norv
32	170.5	8.9	596	11 099NB8	099NB8 mus musculus
33	169	8.8	314	4 09H8R7	09H8R7 homo sapien
34	167.5	8.8	582	11 08R317	08R317 mus musculus
35	167	8.7	638	11 09QZM0	09QZM0 mus musculus
36	165	8.6	589	4 09H3R4	09H3R4 caenorhabd1
37	155.5	8.6	502	5 018672	018672 trypanosoma
38	155.5	8.1	101	5 09GZJ7	09GZJ7 hydractinia
39	155	8.1	915	5 026872	026872 trypanosoma
40	150	7.9	585	13 09PVN8	09PVN8 xenopus lae
41	150	7.9	624	4 09UH09	09UH09 homo sapien
42	150	7.9	624	4 09HAZ4	09HAZ4 homo sapien
43	147.5	7.7	902	10 09FH07	09FH07 arabidopsis
44	140	7.3	701	13 091890	091890 xenopus lae
45	137.5	7.2	349	12 09DP72	09DP72 chlorella v

ALIGNMENTS

RESULT 1
ID Q94CE9 PRELIMINARY; PRT; 365 AA.
AC Q94CE9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative RAD23 protein.
GN F20B17.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP
RA YAMADA K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA YAMADA K., Liu S.X., Quach H.L., Tang C., Toriumi M., Yu G.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G.,
RA Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koeseima E.,
RA Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M.,
RA Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A.,
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT Submitted length of gene F20B17.8 (GI:7715605).";
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
[2]
RP
RA YAMADA K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
RA Yamanura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Kim C., Koeseima E., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene F20B17.8 (GI:7715605).";
RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY034912; AAK59419.1; -;
DR EMBL; AY063103; AAL34277.1; -;

Query	Subject	Similarity	Score	DB	Length
DR InterPro: IPR004806; Rad23.		61.2%	1169.5	DR 10;	365
DR InterPro: IPR000449; UBA_domain.		65.1%		Pred. No.2.6e-72;	
DR InterPro: IPR000626; Ubiqultin.		43;		Mismatches 66;	
DR pfam; PF00627; UBA_2.				Indels 23;	Gaps 9
DR pfam; PF00240; ubiquitin; 1.					
DR TIGRFAMs; TIGR00601; rad23; 1.					
DR PROSITE; PS00053; UBIQUITIN_2; 1.					
DR SEQUENCE 365 AA; 39157 MW; 4FED9EC59B467745 CRC64;					
Query Match					
Best Local Similarity					
Matches 246; Conservative					
DR 1 MKLFTKLTGTFEIRVQPNDTIMAVKKNIEIOGKDSYPMGQQLITNGKYLKDESTLE 60					
Db 1 MKLVTKLTGSHFEIRVLPSDTIMAVKKNIEIDSGKDNTPCGQLILHNGKYLKDESTLV 60					
QY 61 ENKVNEDGLVYMLSKGTSGSTGSSSO--HSNTPAIRQAPPLPAQAOPPPVAPITTT 118					
Db 61 ENKVTKEEGLVYMLSKSGSGAGASVQPVSAITTSSTPAP--STQSSPVPAASPPIA 118					
QY 119 SQPEGLPQAPPTHTNMAANLISGRNVDTIIQLMEMGGSSDKXKVPALPAAYANNPPR 178					
Db 119 QEQ---PAQIDITVQQAASITLVSGSSLEEMVQQLIHMGSGSKDKETVTRALPAANNPPR 175					
QY 179 AVEYLXSGIPVTAELAVP-----IGGQGANITDRAPTGAGLSGIPNTAPLDFPGASN 233					
Db 176 AVDYLYSGIPQAEVAVPVPEAQINGSGA----APVAPA--SGGNSSPLDLPQETVA 228					
QY 234 AGGGAGGGLDRLRNNPQFQANREAVHNPQLQPLVLYELSQNQQLRLIENHDEFLQ 293					
Db 229 AAGSGDLGLTELRNNDDQQLRTVHNSPOLQPLQDELQKONQQLRLIQENQAEFLQ 288					
QY 294 LLINEPEEG--GGCDLIDQPEEDDEMFAISVYPEEQEALIGLESMGFDRAVTEAFACDR 351					
Db 289 LVNEYEESDGGDEGMEDQEQ--EMPHALNVTPEAQEALIQRLFAMGPDRLVTEAFACDR 347					
QY 352 NEELNATLLEHAGE-ED 368					
Db 348 NEELNATLLENSGDFED 365					
RESULT 2					
003991					
ID 003991	PRELIMINARY;			379 AA.	
AC 003991;					
DT 01-JUL-1997 (TREMBLrel. 04, Created)					
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)					
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)					
DE RAD23 protein, isoform II.					
OS Daucus carota (Carrot).					
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;					
OC Asteridae; euasterids II; Apiales; Apiaceae; Daucus.					
NCBI_TaxID=4039;					
NP 11					
RP SEQUENCE FROM N.A.					
RC STRAIN=MD01C.					
RX MEDLINE=98345997; PubMed=9681019;					
RA Sturm A.; Leinhard S.;					
RT "Two isoforms of plant RAD23 complement a UV-sensitive rad23 mutant in					
RL yeast.";					
RU Plant J. 13:815-821(1998).					
DR EMBL; Y12014; CAAT72742.1; -.					
DR HSP; P54725; IDV0.					
DR InterPro; IPR004806; Rad23.					
DR InterPro; IPR000449; UBA_domain.					
DR InterPro; IPR000626; Ubiqultin.					
DR pfam; PF00627; UBA_2.					
DR pfam; PF00240; ubiquitin; 1.					
DR SMART; SM00165; UBA_2.					
DR SMART; SM00213; UBQ; 1.					
DR TIGRFAMs; TIGR00601; rad23; 1.					

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DR PROSITE: PS50053; UID:OJITN1.2; 1
SQ SEQUENCE 379 AA; 40530 MW; B26697BA39CC5929 CRC64;
Query Match 60.4%; Score 1153.5; DB 10; Length 379;
Best Local Similarity 63.0%; Pred. NO. 3.5e-71;
Matches 240; Conservative 45; Mismatches 81; Indels 15; Gaps 9;
OY 1 MKLIVTKTGTHFEETRVQNPDTIMAVKKRIEIOGKDSYPMGOOLLINQKVLKDESTLE 60
DB 1 MKLIVTKTKGSHFEETRAQNPDTIVAIKKNIEDLOSKDNTPCGOOLLINQKVLKDESTLE 60
OY 61 ENKWNEDGFLVYMLSKGTSGSTGTSOSSQHSNTPATROAP--PLEAPQAPQPPVADIT 117
DB 61 ESKISEDGFLVYMLKSKTMSSTGTPAASSAPAPAPAPAPAPAPAPAPAPASAVIDNT 120
OY 118 TSGPQG--LPQAQAP-NTHDNMAASNLISGRNDPTIINOLEMNGGGGWDKXQALRAAYN 174
DB 121 T-VPPAPLSPAPAPAPSDTYGGAASNVVAAASNLIEQTIIQHTMDMGGMWDITNMVSRALRAAYN 179
OY 175 NPERAVEXLYSGIPTATIAIAPD----GQGANVTUDRA--PTGEGALS-GINPTAPLDLFP 228
DB 180 NPERAVDLYSGIPTEMAEAAVPSHFQGDQINAGCNNAISDNCVAGAACARNSLPLNMF 239
OY 229 QGASNAGGAGAGGGLDPTLRNNPQFOGAVREMYHTNPOLLQPMVLVELSKONPOLRLIEENH 288
DB 240 QETLSGVAGAGAGSGSEFEFRNNPQFOETLSKMYQARNPOLLIQPMLELIGKONPOLRLIOEHH 299
OY 289 DEFLLQLEWPEPGCGDLPDDEPEEMHAI5YMPDEBQALIGRLSEMGFDRAVTEARLA 348
DB 300 BEFLQLEWPEVAGSGDGFDPEDQ-VQETITVADQDALETERLEWAGFDKGLVTEAPLA 358
OY 349 CDRNEELANTYLLFNHAGE-ED 368
DB 359 CDRNEELAVNTYLENAGDFED 379
RESULT 3
O9MA10 PRELIMINARY; PRT; 367 AA.
AC O9MA10;
DT 01-OCT-2000 (TREMBLrel. 15, created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE F20B17.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxID=3702;
[1]
RN RP SEQUENCE FROM N.A.
RA Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C.,
RA Shinn P., Altafi H., Bei Q., Chin C., Chlou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J.,
RA Ienz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Theoverl A.,
RA Tortium M., Vaysberg M., Yu G., Federspiel N.A., Theodidis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F20B17 from chromosome
RT 1."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
[3]
RN RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
[4]
RN RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chlou J., Choi E.,

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RA Conn L., Conway A., Gonzalez A., Hansen N., Howling B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharly N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thayer A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.,
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC010793; AF68123.1; -.
DR HSSP: P54725; IDV0.
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA_domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00627; UBA; 2.
DR Pfam: PF00240; ubiquitin; 1.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBO; 1.
DR TIGRFAMs: TIGR00601; rad23; 1.
DR PROSITE: PSS0053; UBIOUITIN_2; 1.
SQ SEQUENCE 367 AA; 39790 MW; C6D0134B5C69CE6 CRC64;

Query Match 54.6%; Score 1043.5; DB 10; Length 367;
Best Local Similarity 59.3%; Pred. No. 1.1e-63;
Matches 232; Conservative 39; Mismatches 73; Indels 47; Caps 11;

QY 1 MKLVKTLKGFHEIRVPNDITMAVKKNIETIGKDSYPMGQOLLFNGKVLDESTLE 60
DB 1 MKLVKTLKGFHEIRVLPDITMAVKKNIETIGKDSYPMGQOLLFNGKVLDESTLV 60
QY 61 ENKYNEDGFLVYMLSKGKSTGSGTSSQ-----HSNTPATROAPPLAQAQAPQPV 113
DB 61 ENKYNEDGFLVYMLSKGKSTGSGTSSQ-----HSNTPATROAPPLAQAQAPQPV 113
QY 114 APIT-----SQPEGLPAQAPNTHDMAANLISGRNVDITINQLEMGGSGMDKDV 165
DB 112 NPVPTSCFTYSGSRITG-----TDYTGQASTLVSGSSLEQWVQQLMEMGGSGMDKDV 166
QY 166 QRALRAVNNPERAVETLYSGIPTAETAP-----IGGCAANTTDRAPTCEAGLSGTPN 220
DB 167 TRALRAVNNPERAVDLYSGIPTAETAVVPEAQAIGASA-----APVAPV--SGGPN 219
QY 221 TAPLDLPPGASNAGGAGGGLDPLFLRNPPQFOAVREKVNHPQILOPMLVELSKONPQI 280
DB 220 SSPDLDFPQEVAAAGSGDGLTEFLRNNDVAIL--TISFSLNCEPMLOELKONPOL 277
QY 281 LRLIENHDEFLOLNEPFEG--GEGDFLDQPEDEMPHAISVTPPEOEAIGRLSEMGFD 338
DB 278 LRLIQEQAQEFLOLVNPEYEGSDGDMFDQPEQ--EMPHAINVPAQEOAIGRLSEMGFD 336
QY 339 RAVTEAFACDRNEELANYLEHAGE--ED 368
DB 337 RALVTEAFACDRNEELANYLEHAGE--ED 367

RESULT 4

Q9STA6 PRELIMINARY; PRT; 389 AA.
AC Q9STA6;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE RAD23 protein.
GN RAD23.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. WEST VIRGINIA 106; TISSUE=FRUIT;
RA Lemaire-Chamley M., Petit J., Raymond P., Chevallier C.;
RT "Analysis of gene expression during early tomato fruit development by
RT mRNA differential display."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ243875; CAB51544.1; -.
DR HSSP: P54725; IDV0.
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA_domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00627; UBA; 2.
DR Pfam: PF00240; ubiquitin; 1.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBO; 1.
DR TIGRFAMs: TIGR00601; rad23; 1.
DR PROSITE: PSS0053; UBIOUITIN_2; 1.
SQ SEQUENCE 389 AA; 41508 MW; D2BAEDFOFE70778A CRC64;

Query Match 53.4%; Score 1019; DB 10; Length 389;
Best Local Similarity 53.8%; Pred. No. 5.9e-62;
Matches 214; Conservative 47; Mismatches 97; Indels 40; Caps 6;

QY 1 MKLVKTLKGFHEIRVPNDITMAVKKNIETIGKDSYPMGQOLLFNGKVLDESTLE 60
DB 1 MKLVKTLKGFHEIRVLPDITMAVKKNIETIGKDSYPMGQOLLFNGKVLDESTLV 60
QY 61 ENKYNEDGFLVYMLSKGKSTGSGTSS-----SOHSTPATROAPPL 102
DB 61 ENKYNEDGFLVYMLSKKRV--STGTSISALSTAPDQSTDAQITTTPTQATLAPQ 119
QY 103 EAPQAPQPVAPPTTSQPEGLPAQAPNTHDMAANLISGRNVDITINQLEMGGSGMDK 162
DB 120 SASASAPTPAPVAPVAPAS-----SYVDVYQASNLVAGSLNETVYQQLDMGGSGMDR 172
QY 163 DKVQALRAVNNPERAVETLYSGIPTAET-----AVPGGCAANTTDRAPT 210
DB 173 DTVVRALFAAVNNPERAVDLYSGIPTAETIPVAPARAAPAVTAPASQAIPNAPQAS 232
QY 211 GEAGLSGIPNTAPLDLPPGASNAGGAGGGLDPLFLRNPPQFOAVREKVNHPQILOPML 270
DB 233 QLAVPSSGPNAPLDLPPGGLTNGSNGAGNLDPLRNSPQFOALRAVQANPQILOPML 292
QY 271 VELSKONPOLRLIENHDEFLOLNEPFEGEGDFLDQPEDEMPHAISVTPPEOEAIG 330
DB 293 QELKQNHMLRLIQEHQPDFLRLINEPVE--GEGNVLQO--TAGALPQAVTTPPEREAIE 350
QY 331 RLESKGFPRAVTEAFACDRNEELANYLEHAGEED 368
DB 351 RLEAMGFDRALVLEVFACNKRNEELANYLEHAGEED 368

RESULT 5

Q9M887 PRELIMINARY; PRT; 419 AA.
AC Q9M887;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Putative RAD23 (At3g02540/F16B3_17).
GN F16B3_17.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA.
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
RA Rensing C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Niernan W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III BAC F16B3 genomic sequence."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Gibson H.A., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,

RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.,
RT "Arabidopsis cDNA clones,"
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC021640; AF32461.1; -
DR EMBL: AY039562; AK62617.1; -
DR HSSP: P54725; IDV0.
DR InterPro: IPR002965; P-rich_extensn.
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA_domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00627; UBA; 2.
DR Pfam: PF00240; ubiquitin; 1.
DR PRINTS: PRO1217; PRICHEXTENS.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBO; 1.
DR TIGRFAMs: TIGR00601; rad23; 1.
DR TrEMBL: P550053; UBIQUITIN_2; 1.
SQ PROSITE: 419 AA; 44247 MW; CAA13BC4FEB1E25 CRC64;

Query Match 51.2% Score 978; DB 10; Length 419;
Best Local Similarity 50.6% Pred No. 4.2e-59;
Matches 213; Conservative 58; Mismatches 90; Indels 60; Gaps 12;

QY 1 MKLTVTLKGTHEIRVQNDITMAVKNIEIOGKDSYPMGQOLLIFNGKYLKDESTLE 60
DB 1 MKLTVTLKGTHEIRVQNDITMAVKNIEIOGKDSYPMGQOLLIFNGKYLKDESTLE 60
QY 61 ENKVNEDGGLVYMLSKGKSGTSSSOHSTPATRQAPPLEAQAPV-----QPPVA- 100
DB 61 ENKVNEDGGLVYMLSKGKSGTSSSOHSTPATRQAPPLEAQAPV-----QPPVA- 100
QY 101 -PLEAFOQAPPEVAP-----ITTSQPEGLPA-----QAP-----NTHDNAASN 138
DB 101 -PLEAFOQAPPEVAP-----ITTSQPEGLPA-----QAP-----NTHDNAASN 138
QY 121 APTRPAPAPPTPAPVAVATEVTTPPIPEPVATISSSTPAPDSAPVSGDGYGGAASN 180
DB 121 APTRPAPAPPTPAPVAVATEVTTPPIPEPVATISSSTPAPDSAPVSGDGYGGAASN 180
QY 139 LLSGRVNTITINOLMEGSGSKDKVQALRAAYNNPERAVEYLTSIGIPVTAETIAVPI- 197
DB 139 LLSGRVNTITINOLMEGSGSKDKVQALRAAYNNPERAVEYLTSIGIPVTAETIAVPI- 197
QY 181 LAGSNLSESTIOOILDMGSGTMDRETIVLALRAAFNNPERAVEYLTSIGIPVTAETIAVPI- 239
DB 181 LAGSNLSESTIOOILDMGSGTMDRETIVLALRAAFNNPERAVEYLTSIGIPVTAETIAVPI- 239
QY 198 -----GGGAGANTTDRAPTEAGISGIPNTAPLIDFPOGASNMGGGAGGPRDPLFRNNPQF 252
DB 198 -----GGGAGANTTDRAPTEAGISGIPNTAPLIDFPOGASNMGGGAGGPRDPLFRNNPQF 252
QY 240 RPPASGGOAPNPAPOOTOPAAPASGPNANPLDLEPOGLPNVNGAGACTDPLFRNSQOF 299
DB 240 RPPASGGOAPNPAPOOTOPAAPASGPNANPLDLEPOGLPNVNGAGACTDPLFRNSQOF 299
QY 253 QAVREKVNHTNPOLPMLVELSKONFOILRIEENHDEFLOLNEPFEKG--EGDFLDQ- 309
DB 253 QAVREKVNHTNPOLPMLVELSKONFOILRIEENHDEFLOLNEPFEKG--EGDFLDQ- 309
QY 300 QALRAVAVQANPQVLPMLDELKONNMLRLIODHQAADFLRLINEVEGGESGNLIGQM 359
DB 300 QALRAVAVQANPQVLPMLDELKONNMLRLIODHQAADFLRLINEVEGGESGNLIGQM 359
QY 310 ----PEEDMPHAISVTPPEQALIGLESMPGFDRAVIEAFLACDRNEELANYLLEHAG 365
DB 310 ----PEEDMPHAISVTPPEQALIGLESMPGFDRAVIEAFLACDRNEELANYLLEHAG 365
QY 366 AAGMPQ-----POAIOVTHEBEAIEERLEAMGFERALVLEVFACNKNNEELANYLLDHMH 415
DB 366 AAGMPQ-----POAIOVTHEBEAIEERLEAMGFERALVLEVFACNKNNEELANYLLDHMH 415
QY 416 E 416

RESULT 6
003990 PRELIMINARY: PRT; 382 AA.
AC 003990:
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE RAD23, isoform 1.
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; easterids II; Apiales; Apiaceae; Daucus.
OX NCBI_TaxID=4039;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M001C;
RX MEDLINE=98345997; PubMed=9681019;
RA Stum A., Leinhard S.; PubMed=9681019;
RT "Two isoforms of plant RAD23 complement a UV-sensitive rad23 mutant in
RT yeast."
RL Plant J. 13:815-821(1998).
DR EMBL: Y12013; CAA72741.1; -
DR HSSP: P54725; IDV0.
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA_domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00627; UBA; 2.
DR Pfam: PF00240; ubiquitin; 1.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBO; 1.
DR TIGRFAMs: TIGR00601; rad23; 1.
DR TrEMBL: P550053; UBIQUITIN_2; 1.
SQ PROSITE: 382 AA; 40344 MW; 27FF02A2402F3DC2 CRC64;

Query Match 49.9% Score 954; DB 10; Length 382;
Best Local Similarity 52.4% Pred No. 1.6e-57;
Matches 205; Conservative 52; Mismatches 98; Indels 36; Gaps 9;

QY 1 MKLTVTLKGTHEIRVQNDITMAVKNIEIOGKDSYPMGQOLLIFNGKYLKDESTLE 60
DB 1 MKLTVTLKGTHEIRVQNDITMAVKNIEIOGKDSYPMGQOLLIFNGKYLKDESTLE 60
QY 61 ENKVNEDGGLVYMLSKGKSGTSSSOHSTPATRQAPPLEAQAPV-----QPPVA- 114
DB 61 ENKVNEDGGLVYMLSKGKSGTSSSOHSTPATRQAPPLEAQAPV-----QPPVA- 114
QY 115 -PITTSQPEGLPAQAP-----NTHDNAASNLLSGRNVDTITINOLMEGSGSKDK 163
DB 115 -PITTSQPEGLPAQAP-----NTHDNAASNLLSGRNVDTITINOLMEGSGSKDK 163
QY 117 LVPPASPPAPAPATAPIPASAAGSEANYSASLLVAGSNLEGAIOOILDMGSGTMDRD 176
DB 117 LVPPASPPAPAPATAPIPASAAGSEANYSASLLVAGSNLEGAIOOILDMGSGTMDRD 176
QY 164 KVQALRAAYNNPERAVEYLTSIGIPVTAETIAVPI-----GGGAGANTTDRAPTG--EAGLS 216
DB 164 KVQALRAAYNNPERAVEYLTSIGIPVTAETIAVPI-----GGGAGANTTDRAPTG--EAGLS 216
QY 177 TVIRIVRAAFNNPERAVEYLTSIGIPVTAETIAVPI-----GGGAGANTTDRAPTG--EAGLS 235
DB 177 TVIRIVRAAFNNPERAVEYLTSIGIPVTAETIAVPI-----GGGAGANTTDRAPTG--EAGLS 235
QY 217 GIPNTAPLIDFPOGASNMG--GGAGGPRDPLFRNNPQFQAVREKVNHTNPOLPMLVELSK 275
DB 217 GIPNTAPLIDFPOGASNMG--GGAGGPRDPLFRNNPQFQAVREKVNHTNPOLPMLVELSK 275
QY 236 ACPNANPLDLEPOGLPDMKSNAGANLDELRTNOQFALRLMVOSNPQIILPMLDELIGK 295
DB 236 ACPNANPLDLEPOGLPDMKSNAGANLDELRTNOQFALRLMVOSNPQIILPMLDELIGK 295
QY 276 QNPOLRLIEENHDEFLOLNEPFEKGEGDFLDQPEEDMPHAISVTPPEQALIGLESMP 335
DB 276 QNPOLRLIEENHDEFLOLNEPFEKGEGDFLDQPEEDMPHAISVTPPEQALIGLESMP 335
QY 296 QNPMLRLIOHQADFLQLINEPMEGENTL-----GGGPOAISVTPPEQALIGLESMP 349
DB 296 QNPMLRLIOHQADFLQLINEPMEGENTL-----GGGPOAISVTPPEQALIGLESMP 349
QY 336 GFDRAVIEAFLACDRNEELANYLLEHAG 366
DB 336 GFDRAVIEAFLACDRNEELANYLLEHAG 366
QY 350 GFDRELVLEVFACNKNNEELANYLLDHMH 380
DB 350 GFDRELVLEVFACNKNNEELANYLLDHMH 380

RESULT 7
09FF16 PRELIMINARY: PRT; 378 AA.
AC 09FF16:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE DNA repair protein RAD23 homolog (Hypothetical 40.1 kDa protein)
DE (At5g38470/At5g38470).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=97471969; PubMed=9330910;
RA Sato S., Kotani H., Nakamura T., Kaneko T., Asamizu E., Fukami M.,

RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
RT features of the 1.6 Mb regions covered by twenty physically assigned
RT pl clones."
RL DNA Res. 4:215-230(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones";
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J.,
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones";
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: AB005248; BAB09359.1; -
DR EMBL: AY058196; AL25609.1; -
DR EMBL: AY081835; AL87405.1; -
DR HSSP: P54725; IDV0.
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA.domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00627; UBA; 2.
DR Pfam: PF00240; ubiquitin; 1.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBO; 1.
DR TIGRFAMs: TIGR00601; rad23; 1.
DR PROSITE: PSS0053; UBQUITIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 378 AA; 40066 MW; DD9B59153EA3E6A9 CRC64;

Query Match 48.8%; Score 931.5; DB 10; Length 378;
Best Local Similarity 52.6%; Pred. No. 5.5e-56;
Matches 200; Conservative 56; Mismatches 109; Indels 15; Gaps 8;

QY 1 MKLVTKLKGTHFEIRVQPNDTIMAVKKNIEIGKDSYPMGQOLLIFNGKVLKDESTLE 60
DB 1 MKIVTKLGSNFEIEVKPADKVDVKATIEYVGAE-YPAKQMLIHQGVLDDEITLE 59
QY 61 ENKYNEDGFLVLMISKGTSGTSSQSHNTPATROAPPLEAP-QQAPOPVAPI 116
DB 60 ENNVNENFIVIMLSKTRKSPGASSTASAPASATOPQVATPVASPTASVPPTSGTA 119
QY 117 TTSOPEGIPAOAPNTHNNAASNLISGRNVDITINQIMEMGGSGMDKQVQALRAAYNP 176
DB 120 TAAAPATAASVQTDVYVGAASNLVAGTLESTVOOILDMGGSGMDRDTIVVALLAAAFNNP 179
QY 177 ERAVEYLSGIPVTAET-TPDRAPTEGAGLSIPTAPLDLFPQ 229
DB 180 ERAVEYLSGIPVTAETIPVQAQAPATGEOANPLAOPQAAAAPAAATGGPAPNPLNLFPO 239
QY 230 GASNAGGAGGGLPDLFNNPQFAVREMTNPOILOPMLVELSKNPQILRIEENHD 289
DB 240 GMPAADAGAGNGNDLFNNSQFOALRAMVQANPOILOPMLQELGKQNPQVRLIQEHOA 299
QY 290 EFLQLNPEPGEDELDQPEDEMPHAISVTPBEQFAIRLSMGDFRARVTEAFIAC 349
DB 300 DFLRLINEPVE-GEENVEQLEA-AMPOAVTVEBEREAIERLBMGDFRAMVLEVFAC 357

QY 350 DRNEELANYLLEHAGE-ED 368
DB 358 KNNEELANYLLDHMHFEED 377

RESULT 8
ID 094C35 PRELIMINARY; PRT; 378 AA.
AC 094C35;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Hypothetical 40.1 KDa protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702.
RN [1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Shinn P.,
RA Tracy S.E., Banh J., Bowser L., Carninci P., Chung M.K.,
RA Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L.,
RA Sakano H., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,
RA Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones";
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: AY037181; AAK5976.1; -
DR EMBL: AY037181; AAK5976.1; -
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA.domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00627; UBA; 2.
DR Pfam: PF00240; ubiquitin; 1.
DR TIGRFAMs: TIGR00601; rad23; 1.
DR PROSITE: PSS0053; UBQUITIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 378 AA; 40075 MW; E49B591527A3EC27 CRC64;

Query Match 48.7%; Score 930.5; DB 10; Length 378;
Best Local Similarity 52.6%; Pred. No. 6.5e-56;
Matches 200; Conservative 56; Mismatches 109; Indels 15; Gaps 8;

QY 1 MKLVTKLKGTHFEIRVQPNDTIMAVKKNIEIGKDSYPMGQOLLIFNGKVLKDESTLE 60
DB 1 MKIVTKLGSNFEIEVKPADKVDVKATIEYVGAE-YPAKQMLIHQGVLDDEITLE 59
QY 61 ENKYNEDGFLVLMISKGTSGTSSQSHNTPATROAPPLEAP-QQAPOPVAPI 116
DB 60 ENNVNENFIVIMLSKTRKSPGASSTASAPASATOPQVATPVASPTASVPPTSGTA 119
QY 117 TTSOPEGIPAOAPNTHNNAASNLISGRNVDITINQIMEMGGSGMDKQVQALRAAYNP 176
DB 120 TAAAPATAASVQTDVYVGAASNLVAGTLESTVOOILDMGGSGMDRDTIVVALLAAAFNNP 179
QY 177 ERAVEYLSGIPVTAET-TPDRAPTEGAGLSIPTAPLDLFPQ 229
DB 180 ERAVEYLSGIPVTAETIPVQAQAPATGEOANPLAOPQAAAAPAAATGGPAPNPLNLFPO 239
QY 230 GASNAGGAGGGLPDLFNNPQFAVREMTNPOILOPMLVELSKNPQILRIEENHD 289
DB 240 GMPAADAGAGNGNDLFNNSQFOALRAMVQANPOILOPMLQELGKQNPQVRLIQEHOA 299
QY 290 EFLQLNPEPGEDELDQPEDEMPHAISVTPBEQFAIRLSMGDFRARVTEAFIAC 349
DB 300 DFLRLINEPVE-GEENVEQLEA-AMPOAVTVEBEREAIERLBMGDFRAMVLEVFAC 357
QY 350 DRNEELANYLLEHAGE-ED 368
DB 358 KNNEELANYLLDHMHFEED 377

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RESULT 9
ID Q40742 PRELIMINARY; PRT; 392 AA.
AC Q40742;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE OSRAD23.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
NCBI_TaxID=4530;
RN
  (1)
  RC SEQUENCE FROM N.A.
  RC STRAIN=NIPPONBARE;
  RX MEDLINE=97369378; PubMed=9225866;
  RA Schultz T.F., Quatrano R.S.;
  RT "Characterization and expression of a rice RAD23 gene.";
  RL Plant Mol. Biol. 34:557-562(1997).
  DR EMBL; 063530; AAB5841.1; -.
  DR HSSP; P54725; IDV0.
  DR InterPro; IPR004486; Rad23.
  DR InterPro; IPR000626; Ubiquitin.
  DR Pfam; PF00627; UBA; 2.
  DR Pfam; PF00240; ubiquitin; 1.
  DR SMART; SM00165; UBA; 2.
  DR SMART; SM00213; UBO; 1.
  DR TIGRFAMs; TIGR00601; rad23; 1.
  DR PROSITE; PS50053; UBQUITIN_2; 1.
  DR PROSITE; PS50053; UBQUITIN_2; 1.
  SQ SEQUENCE 392 AA; 41754 MW; BDE08574CCTACB CRC64;

Query Match
Best Local Similarity 46.5%; Score 887.5; DB 10; Length 392;
Best Local Similarity 50.9%; Pred. No. 6e-53;
Matches 199; Conservative 52; Mismatches 109; Indels 31; Gaps 10;

OY 1 MKLTVTKLGTFFELRVOPNDTMAVKKNIIEIIGKDSYPMGQQLIFNGKYLKDESTLE 60
DB 1 MKISVTKLGSTFEIIVDSAKVADVKRIETTGQGHIVPAEQOMLIHQGKVLKDDTLD 60
OY 61 ENKVNEDGFLVYMLSKGTSGTSSQHSNTPATROAPLEAPQAP--QPPVAPITT 118
DB 61 ENKVNEDGFLVYMLSKGTSGTSSQHSNTPATROAPLEAPQAP--QPPVAPITT 118
OY 119 -----SQEGFLPAQAP-----NTHDNAANLLSGRNVDTIINOLMEGGSGMDK 163
DB 117 VEVTVSAPPTTATSPAPAVAVSSADNTGQATSNLVAAGSNLEATIGLMEGGGIMDD 176
OY 164 KVORALRAAYNNPERAVEYLYSGIPYTAETAVPIGG--QGANTTDR-----PTGEAGLSGI 218
DB 177 IYVHAISAFAFNPERAVEYLYSGVPEQMDIPVPPSIQNPANPTQASQATQAPAPSTLSSG 236
OY 219 PHTAPLDEPQASNAGGAGG--GPLDFLRNPPQQAQVEMVHTNQITQPMVLVELSKN 277
DB 237 PNASPLDLPQALPNASTDAAGLGNIDALRNNAQFETLLSLVQANQIILQPLQELGKGN 296
OY 278 PQILRLIEENHDEFLQILNEPEEG--GEGDFLDQ--PEDEMPHAI SVTPPEOFAIGLEEM 335
DB 297 PQILOLQIGNQAEFLALINEPAEGDDEMLDQFPF--AMPQTIATVPDEDAIILRLPM 354
OY 336 GEDRAVIEAPLACDRNEELANLYLEHAGE 366
DB 355 GEDRALVLDVFFACNKDEQLAANYLLDHMNE 385

RESULT 10
ID Q9S9L8 PRELIMINARY; PRT; 246 AA.
AC Q9S9L8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

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DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE T24D18.27 protein.
GN T24D18.27.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
RN
  (1)
  RC SEQUENCE FROM N.A.
  RC STRAIN=CV. COLUMBIA;
  RA Liu S.X., Yu G., Sakano H., Jhaveri A., Lee J.M., Lenz C., Pham P.,
  RA Toriumi M., Chin C., Chlou J., Choi E., Chung M., Gonzalez A.,
  RA Howing B., Koo T., Li J., Liu A., Vaysberg M., Altati H., Brooks S.,
  RA Buehler E., Chao Q., Conn L., Conway A., Hansen N., Johnson-Hopson C.,
  RA Khan S., Kim C., Lam B., Nguyen M., Palm C., Shinn P., Tambunga G.,
  RA Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
  RT "The sequence of BAC T24D18 from Arabidopsis thaliana chromosome 1.";
  RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
  RN
  (2)
  RC SEQUENCE FROM N.A.
  RC STRAIN=CV. COLUMBIA;
  RA Theologis A.;
  RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
  DR EMBL; AC010924; AAF18513.1; -.
  DR HSSP; P02248; IUBI.
  DR InterPro; IPR000449; UBA_domain.
  DR InterPro; IPR000626; Ubiquitin.
  DR Pfam; PF00627; UBA; 1.
  DR Pfam; PF00240; ubiquitin; 1.
  DR SMART; SM00165; UBA; 1.
  DR SMART; SM00213; UBO; 1.
  DR PROSITE; PS50053; UBQUITIN_2; 1.
  DR PROSITE; PS50053; UBQUITIN_2; 1.
  SQ SEQUENCE 246 AA; 25966 MW; 0867D1E7D72B6FFE CRC64;

Query Match
Best Local Similarity 34.6%; Score 661.5; DB 10; Length 246;
Best Local Similarity 36.7%; Pred. No. 9.5e-38;
Matches 143; Conservative 29; Mismatches 63; Indels 17; Gaps 4;

OY 1 MKLTVTKLGTFFELRVOPNDTMAVKKNIIEIIGKDSYPMGQQLIFNGKYLKDESTLE 60
DB 1 MKLTVTKLGSFELRVLPDTIMAVKKNIEDSOKDNTPCGOQLIFNGKYLKDESTLV 60
OY 61 ENKVNEDGFLVYMLSKGTSGTSSQHSNTPATROAPLEAPQAPQPPVAPITT 120
DB 61 ENKVNEDGFLVYMLSKGTSGTSSQHSNTPATROAPLEAPQAPQPPVAPITT 120
OY 121 PEGLRQAPNTDANASNLSSGRNVDTIINOLMEGGSGMDKQVORALRAAYNNPERAV 180
DB 109 VOEOPTAOSDTYGOAASLTSSGSSIEOMVOQIMEMGGSGMDKETVTRALRAAYNNPERAV 168
OY 181 EYVSGIPYTAET--AVPIGGAGNTTDRAPTEAGLISGIPNAPLDEPQASNAGGAG 239
DB 169 DYVSGIPETVYIPATNLSGVSGRELTRAPP-----SGPNSPLDLPQEA VSDAAGD 224
OY 240 GGPLDFLRNPPQ 251
DB 225 LCTLEFLRNGNDQ 236

RESULT 11
ID Q8WUB0 PRELIMINARY; PRT; 409 AA.
AC Q8WUB0;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE RAD23 homolog B (S. cerevisiae).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID=9606;
RN
  (1)

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RP SEQUENCE FROM N.A.
RC TISSUE-UTERUS;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC020973: AAH20973.1; -
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA_domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00627; UBA; 2.
DR Pfam: PF00240; ubiquitin; 1.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBA; 1.
DR TIGRPFAMs: TIGR00601; rad23; 1.
DR PROSITE: PSS0053; UBQUITIN_2; 1.
SQ SEQUENCE 409 AA; 43199 MW; 475FED499DACAC69 CRC64;

Query Match 32.5%; Score 621.5; DB 4; Length 409;
Best Local Similarity 34.6%; Pred. No. 1,le-34;
Matches 146; Conservative 83; Mismatches 126; Indels 67; Gaps 11;

DY 1 MKLVTKLKGTHFEIRVOPNDTMAVKKNIEIGKDSYPMGOQLIFNGKVLDESTLE 60
Dd 1 MIVTLKLGQOTFTIEDIDPETVAKLEKIESEKGAFFVAGKLIYAGILDDRTVG 60
DY 61 ENKYNEDGFLVYMLSKGT-----SGSTGSSSHSNTPATRQAP--PLEAPQ 106
Dd 61 EYKIDENKFFVYMLTRDSSSNRQOLSYKESNKLITSTDSSKQMPCEANHTNSPSTNT 120
DY 107 QAP-----QVAPITTSOPEGLPAQAP-----NTIDNA 135
Dd 121 STPASTPASTVASSSEAPASAKOEKPAEKPAETPAVTSPTAVDTSIGSSRSNLEDA 180
DY 136 ASNLISGRNVDITINQLEMGGSGMDKQVORALAAVNNPERAVEYLVSIGPYTAET-A 194
Dd 181 TSAVYTGSTENMYTEIMSKG---YEREQVIALRAFSENNDRAVEYILMIIPDREQA 237
DY 195 VPIGGGANTTDRAPTEBAGISGIPNTAPDLFPGGASNAGGAGGGLDFLRNNPOQA 254
Dd 238 VVDPPOQAST--GVPOSSAVAAAAATTT-----ATTTTSSGGHLEFLRNQPOQ 287
DY 255 VREAVHNPOILQPMVLELSONPOILRLIENHDEFQLINPEP-----GGEGDLD 308
Dd 288 MKQILQONPSLIPALLOOIGRENPOLOOISOHQEHFLOMNEVQAEAGGGGGGGSG 347
DY 309 QPEDEMPHA--ISVTEEOEAGRLSMGFDRARVIEAFLACRNEELIANYLLEHAGE 366
Dd 348 GIAVAGSHMYIQVTEQEKALIRKALGFPREGVITQAYACKEKNEVLNANFLIQNFD 407
DY 367 ED 368
Dd 408 ED 409

RESULT 12
Q9XZE0 PRELIMINARY; PRT; 414 AA.
AC Q9XZE0;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE DHR23.
GN RAD23 OR CG1836.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Eurygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Nblirchikina E.N., Grischuk A.L., Soldatov A.V.;
RT "Cloning and characterization of the Drosophila melanogaster homologue
RL Genetika 35:0-0(1999).

DR EMBL: AF136606; AAD33695.1; -
DR HSSP: P54725; IDV0.
DR FlyBase: FBgn0026777; Rad23.
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA_domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00627; UBA; 2.
DR Pfam: PF00240; ubiquitin; 1.
DR PRINTS: PR01574; TUBBYPROTEIN.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBA; 1.
DR TIGRPFAMs: TIGR00601; rad23; 1.
DR PROSITE: PSS0053; UBQUITIN_2; 1.
SQ SEQUENCE 414 AA; 45794 MW; 4C2FF94C1167AB CRC64;

Query Match 25.7%; Score 490.5; DB 5; Length 414;
Best Local Similarity 29.0%; Pred. No. 1e-25;
Matches 129; Conservative 77; Mismatches 130; Indels 109; Gaps 11;

DY 1 MKLVTKLKGTHFEIRVOPNDTMAVKKNIEIGKDSYPMGOQLIFNGKVLDESTLE 60
Dd 1 MIVTLKLGQOTFTIEFAPEKTVLEIKKIEERNGPE-YVAEKGLIYAGIYLLDDRTVG 59
DY 61 ENKYNEDGFLVYMLSKGTSGSTGSSSHSN---TPATRQAPPLAPQAPQAP----- 111
Dd 60 SYNVDKFFVYMLTRDSSSNRQOLSYKESNKLITSTDSSKQMPCEANHTNSPSTNT 119
DY 112 -----PVAPITTSOPEGLPAQAPNTHDNAVNLGSRNVDITINQLEMGGSGMDK 164
Dd 120 EDSVLSRETRPLSDELIGELAQ-A-SLOSRAESNLMKDEYVNLGVLSEVNG--YPREQ 175
DY 165 VORALRAVNNPERAVEYLVSIGPY-----TAETAVPIGGGANTTDRAPTE 212
Dd 176 VERMAASVNNPERAVEYLINGIPAEGETFYNRLESTNPGLISGPPASATSAENSTE 235
DY 213 AGLSGIPNTAPDLFPGGASNAGGAGGGLDFLRNNPOQAVEMVHTNPQILQPMVE 272
Dd 236 -----SNDDPREFLRSQPOFLMRSLAYONPHLLHAVLOQ 270
DY 273 LSKONPOLRLIENHDEFQLINPEP-----EGG----- 302
Dd 271 IGQNPALQILISENODFLMLNPOPIDRESECATYVPVSNARIPTSLDNDVLFSPDLE 330
DY 303 -----EGDPLDQPEDEMPHAIS--VPREEOEAGRLSMGFDRARV 342
Dd 331 VATSAQNSAGTSAHQSGAADN-EDLEQPLGVSTILNQNDDALIRKALFEPEALV 389
DY 343 IEAFLACRNEELIANYLLEHAGE 367
Dd 390 LQAYFACEKNEEOANFLSSSFFD 414

RESULT 13
Q9V3W9 PRELIMINARY; PRT; 414 AA.
AC Q9V3W9;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE RAD23 protein.
GN RAD23 OR CG1836.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Eurygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaratides P.G., Scherier S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

[illegible]

